

SEQUENCE LISTING

<110> Pangalos, Menelas
Neefs, Jean-Marc
Peeters, Danielle

<120> Cloning and Characterisation of Novel Mammalian Peptidases

<130> J0205/7000 (JRV)

<140> 09/743,647

<141> 2001-01-12

<150> GB 9815284.6

<151> 1999-07-14

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<170> PatentIn version 3.0

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<212> PRT

<213> Homo sapiens

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<222> (100)..(100)

<223> Xaa is unknown

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 Asn Ser Leu Ala Pro Gln Asp Leu Asp Leu Glu Ile Leu Glu Thr Val
 35 40 45
 Met Gly Gln Leu Asp Ala His Arg Ile Arg Glu Asn Leu Arg Glu Leu
 50 55 60
 Ser Arg Glu Pro His Leu Ala Ser Ser Pro Arg Asp Glu Asp Leu Val
 65 70 75 80
 Gln Leu Leu Leu Gln Arg Trp Lys Asp Pro Glu Ser Gly Leu Asp Ser
 85 90 95
 Ala Glu Ala Xaa Thr Tyr Glu Val Leu Leu Ser Phe Pro Ser Gln Glu

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Ser	Cys	His	Arg	Thr	Glu	Glu	Asn	Val	Thr	Gly	Glu	Gln	Gly	Gly	Pro		
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Asp	Val	Val	Gln	Pro	Tyr	Ala	Ala	Tyr	Ala	Pro	Ser	Gly	Thr	Pro	Gln		
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			180					185					190				
Tyr	Gly	Gly	Val	Gly	Arg	Gly	Ala	Lys	Ala	Val	Asn	Ala	Ala	Lys	His		
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Gly	Val	Ala	Gly	Val	Leu	Val	Tyr	Thr	Asp	Pro	Ala	Asp	Ile	Asn	Asp		
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Pro	Ser	Gly	Val	Glu	Arg	Gly	Ser	Tyr	Tyr	Glu	Tyr	Phe	Gly	Asp	Pro		
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Leu	Thr	Pro	Tyr	Leu	Pro	Ala	Val	Pro	Ser	Ser	Phe	Arg	Val	Asp	Leu		
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		275					280					285					
Gln	Asp	Ala	Arg	Asp	Leu	Leu	Cys	Asn	Leu	Asn	Gly	Thr	Leu	Ala	Pro		
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Phe	Arg	Pro	Asp	Gly	Asp	Phe	Pro	Ala	Asp	Ser	Gln	Val	Asn	Val	Ser		
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Val	Tyr	Asn	Arg	Leu	Glu	Leu	Arg	Asn	Ser	Ser	Asn	Val	Leu	Gly	Ile		
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Ile	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Leu	Tyr	Gly	Asn	His		
		355					360					365					
Arg	Asp	Ser	Trp	Val	His	Gly	Ala	Val	Asp	Pro	Ser	Ser	Gly	Thr	Ala		
	370					375					380						
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Thr	Trp	Arg	Pro	Arg	Arg	Ser	Ile	Val	Phe	Ala	Ser	Trp	Gly	Ala	Glu		
				405					410					415			

Glu	Phe	Gly	Leu	Ile	Gly	Ser	Thr	Glu	Phe	Thr	Glu	Glu	Phe	Phe	Asn	420	425	430
Lys	Leu	Gln	Glu	Arg	Thr	Val	Ala	Tyr	Ile	Asn	Val	Asp	Ile	Ser	Val	435	440	445
Phe	Ala	Asn	Ala	Thr	Leu	Arg	Val	Gln	Gly	Thr	Pro	Pro	Val	Gln	Ser	450	455	460
Val	Val	Phe	Ser	Ala	Thr	Lys	Glu	Ile	Arg	Ser	Pro	Gly	Pro	Gly	Asp	465	470	475
Leu	Ser	Ile	Tyr	Asp	Asn	Trp	Ile	Arg	Tyr	Phe	Asn	Arg	Ser	Ser	Pro	485	490	495
Val	Tyr	Gly	Leu	Val	Pro	Ser	Leu	Gly	Ser	Leu	Gly	Ala	Gly	Ser	Asp	500	505	510
Tyr	Ala	Pro	Phe	Val	His	Phe	Leu	Gly	Ile	Ser	Ser	Met	Asp	Ile	Ala	515	520	525
Tyr	Thr	Tyr	Asp	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Ile	Tyr	Pro	Thr	Tyr	530	535	540
His	Thr	Ala	Phe	Asp	Thr	Phe	Asp	Tyr	Val	Asp	Lys	Phe	Leu	Asp	Pro	545	550	555
Gly	Phe	Ser	Ser	His	Gln	Ala	Val	Ala	Arg	Thr	Ala	Gly	Ser	Val	Ile	565	570	575
Leu	Arg	Leu	Ser	Asp	Ser	Phe	Phe	Leu	Pro	Leu	Lys	Val	Ser	Asp	Tyr	580	585	590
Ser	Glu	Thr	Leu	Arg	Ser	Phe	Leu	Gln	Ala	Ala	Gln	Gln	Asp	Leu	Gly	595	600	605
Ala	Leu	Leu	Glu	Gln	His	Ser	Ile	Ser	Leu	Gly	Pro	Leu	Val	Thr	Ala	610	615	620
Val	Glu	Lys	Phe	Glu	Ala	Glu	Ala	Ala	Ala	Leu	Gly	Gln	Arg	Ile	Ser	625	630	635
Thr	Leu	Gln	Lys	Gly	Ser	Pro	Asp	Pro	Leu	Gln	Val	Arg	Met	Leu	Asn	645	650	655
Asp	Gln	Leu	Met	Leu	Leu	Glu	Arg	Thr	Phe	Leu	Asn	Pro	Arg	Ala	Phe	660	665	670
Pro	Glu	Glu	Arg	Tyr	Tyr	Ser	His	Val	Leu	Trp	Ala	Pro	Ser	His	Gly	675	680	685
Leu	Arg	Ser	His	Ile	Pro	Gly	Leu	Ser	Asn	Ala	Cys	Ser	Arg	Ala	Arg	690	695	700
Asp	Thr	Ala	Ser	Gly	Ser	Glu	Ala	Trp	Ala	Glu	Val	Gln	Arg	Gln	Leu	705	710	715
Ser	Ile	Val	Val	Thr	Ala	Leu	Glu	Gly	Ala	Ala	Ala	Thr	Leu	Arg	Pro	725	730	735

Val Ala Asp Leu
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<210> 36

<211> 745

<212> PRT

<213> Rattus rattus

<400> 36

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35 40 45

Ile Leu Asp Ser Val Met Gly Gln Leu Asp Ala Ser Arg Ile Arg Glu
50 55 60

Asn Leu Arg Glu Leu Ser Lys Glu Pro His Val Ala Thr Ser Ala Arg
65 70 75 80

Asp Glu Ala Leu Val Gln Leu Leu Leu Gly Arg Trp Lys Asp Ser Ala
85 90 95

Ser Gly Leu Asp Thr Ala Lys Thr Tyr Glu Tyr Thr Val Leu Leu Ser
100 105 110

Phe Pro Ser Thr Glu Gln Pro Asn Ser Val Glu Val Val Gly Pro Asn
115 120 125

Gly Thr Val Phe His Ser Phe Gln Pro Phe Glu Lys Asn Leu Thr Gly
130 135 140

Glu Gln Ala Glu Pro Asn Val Leu Gln Pro Tyr Ala Ala Tyr Ala Pro
145 150 155 160

Pro Gly Thr Pro Lys Gly Pro Leu Val Tyr Ala Asn Arg Gly Ser Glu
165 170 175

Asp Asp Phe Lys Lys Leu Glu Ala Glu Gly Ile Asn Leu Lys Gly Thr
180 185 190

Ile Ala Leu Thr Arg Tyr Gly Ser Val Gly Arg Gly Ala Lys Ala Ile
195 200 205

Asn Ala Ala Arg His Gly Val Val Gly Val Leu Val Tyr Thr Asp Pro
210 215 220

Gly Asp Ile Asn Asp Gly Lys Ser Leu Pro Asn Glu Thr Phe Pro Asn

225		230		235		240
Ser Trp Gly Leu	Pro 245	Pro Ser Gly Val	Glu 250	Arg Gly Ser Tyr	Tyr 255	Glu
Tyr Phe Gly Asp	Pro 260	Leu Thr Pro	Tyr 265	Leu Pro Ala His	Pro 270	Val Ser
Phe Arg Leu Asp	Pro 275	His Asn Ile	Ser 280	Gly Phe Pro	Pro 285	Ile Pro Thr
Gln Pro Ile Gly	Phe 290	Glu Asp Ala	Lys 295	Asn Leu Leu	Cys 300	Asn Leu Asn
Gly Thr Ser Ala	Pro 310	Asp Ser Trp	Gln 315	Gly Ala Leu	Gly Cys Glu	Tyr 320
Lys Leu Gly Pro	Gly 325	Phe Glu Pro	Asn 330	Gly Asn Phe	Pro 335	Ala Gly Ser
Glu Val Lys Val	Ser 340	Val Tyr Asn	Arg 345	Leu Glu Leu	Arg 350	Asn Ser Ser
Asn Val Leu Gly	Ile 355	Ile Gln Gly	Ala 360	Val Glu Pro	Asp 365	Arg Tyr Val
Ile Tyr Gly Asn	His 370	Arg Asp Ser	Trp 375	Val His Gly	Ala 380	Val Asp Pro
Ser Ser Gly Thr	Ala 385	Val Leu Leu	Glu 390	Ile Ser Arg	Val 395	Leu Gly Thr
Leu Leu Lys Lys	Gly 405	Thr Trp Arg	Pro 410	Arg Arg Ser	Ile 415	Ile Phe Ala
Ser Trp Gly Ala	Glu 420	Glu Phe Gly	Leu 425	Ile Gly Ser	Thr 430	Glu Phe Thr
Glu Glu Phe Leu	Ser 435	Lys Leu Gln	Glu 440	Arg Thr Val	Thr 445	Tyr Ile Asn
Val Asp Ile Ser	Val 450	Phe Ser Asn	Ala 455	Thr Leu Arg	Ala 460	Gln Gly Thr
Pro Pro Val Gln	Ser 465	Val Ile Phe	Ser 470	Ala Thr Lys	Glu 475	Ile Ser Ala
Pro Gly Ser Ser	Gly 485	Leu Ser Ile	Tyr 490	Asp Asn Trp	Ile 495	Arg Tyr Thr
Asn Arg Ser Ser	Pro 500	Val Tyr Gly	Leu 505	Val Pro Ser	Met 510	Gly Thr Leu
Gly Ala Gly Ser	Asp 515	Tyr Ala Ser	Phe 520	Ile His Phe	Leu 525	Gly Ile Thr
Ser Met Asp Leu	Ala 530	Tyr Thr Tyr	Asp 535	Arg Ser Lys	Thr 540	Ser Ala Arg

Ile Tyr Pro Thr Tyr His Thr Ala Phe Asp Thr Phe Asp Tyr Val Glu
545 550 555 560

Lys Phe Leu Asp Pro Gly Phe Ser Ser His Gln Ala Val Ala Arg Thr
565 570 575

Ala Gly Ser Val Leu Leu Arg Leu Ser Asp Ser Leu Phe Leu Pro Leu
580 585 590

Asn Val Ser Asp Tyr Ser Glu Thr Leu Gln Ser Phe Leu Gln Ala Ala
595 600 605

Gln Glu Asn Leu Gly Ala Leu Leu Glu Ser His Asn Ile Ser Leu Gly
610 615 620

Pro Leu Val Thr Ala Val Glu Lys Phe Lys Ala Ala Ala Ala Ala Leu
625 630 635 640

Asn Gln His Ile Leu Thr Leu Gln Lys Ser Ser Pro Asp Pro Leu Gln
645 650 655

Val Arg Met Val Asn Asp Gln Leu Met Leu Leu Glu Arg Ala Phe Leu
660 665 670

Asn Pro Arg Ala Phe Pro Glu Glu Arg Tyr Tyr Ser His Val Leu Trp
675 680 685

Ala Pro Asn Thr Ala Ser Val Ala Thr Phe Pro Gly Leu Ala Asn Ala
690 695 700

Tyr Ala Arg Ala Gln Glu Ile Asn Ser Gly Ala Glu Ala Trp Ala Glu
705 710 715 720

Val Glu Arg Gln Leu Ser Ile Ala Val Met Ala Leu Glu Gly Ala Ala
725 730 735

Ala Thr Leu Gln Pro Val Thr Asp Leu
740 745

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<211> 41

<212> PRT

<213> Homo sapiens

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Tyr Gly Gly Val Gly Arg Gly Ala Lys
35 40

<210> 38

<211> 35

<212> PRT

<213> Homo sapiens

<400> 38

Cys Asn Leu Asn Gly Thr Leu Ala Pro Ala Thr Trp Gln Gly Ala Leu
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Gly Cys His Tyr Arg Leu Gly Pro Gly Phe Arg Pro Asp Gly Asp Phe
20 25 30
Pro Ala Asp
35

<210> 39

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<213> Homo sapiens

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1 5 10 15
Ser Pro Ala Gln
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<210> 40

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<212> PRT

<213> Homo sapiens

<400> 40

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20 25 30
Arg Leu Trp Pro Gly Gln Arg Gly Val

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<211> 229

<212> DNA

<213> Homo sapiens

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tctggatgcc gctgtcctca tccagccctg cccttgccac caccagccc agctccccct 180
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<213> Homo sapiens

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Gly Cys Arg Cys Pro His Pro Ala Leu Pro Leu Pro Pro Pro Ser Pro
20 25 30
Ala Pro Pro Ala His Leu Ser Leu Ser Ser Gly Ser Leu Pro Leu Phe
35 40 45
Leu Trp Pro
50

<210> 43

<211> 82

<212> DNA

<213> Homo sapiens

<400> 43

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82

<210> 44

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1 5 10 15

Asp

<210> 45

<211> 74

<212> DNA

<213> Homo sapiens

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cttgttcttc acag 74

<210> 46

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<213> Homo sapiens

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Gly Met His Ser Pro Asp Pro Glu Val Trp Gly Ala Leu His Pro His
1 5 10 15

Asp

<210> 47

<211> 3110

<212> DNA

<213> Homo sapiens

<400> 47

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caaccacttc tgtgcgctat catcaaagta tacgggtggaa actggtatcc gaaatgaaag	180
ctgaaaacat caaatcatth cttcgttctt ttacaaagct tcctcatctg gcaggaacag	240
aacaaaattt cttgcttgcc aagaaaatcc aaaccagtg gaagaaattt ggactagatt	300
cagccaagtt ggttcattat gatgtcctct tatcttacc caatgagaca aatgccaaact	360
atatatcgat tgtggatgaa catgaaactg agattttcaa aacatcatac cttgaaccac	420
caccagatgg ctatgagaat gttacaaata ttgtgccacc atataatgct ttctcagccc	480
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aactagaaag agagatgggc atcaactgta ctgggaagat tgttattgca agatatggaa	600
aatctttcag aggaaataaa gttaaaaatg ccatgttagc aggagccata ggaatcatct	660
tgtactcaga tccagctgac tactttgctc ctgaggtaca gccatatccc aaaggatgga	720
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gctacttggg aggaattgct ccaccagata agagttggaa gggagccctt aatgtgagtt	960
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<210> 48

<211> 740

<212> PRT

<213> Homo sapiens

<400> 48

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			20					25					30			
Pro	Leu	Lys	Glu	Thr	Thr	Thr	Ser	Val	Arg	Tyr	His	Gln	Ser	Ile	Arg	
		35					40					45				
Trp	Lys	Leu	Val	Ser	Glu	Met	Lys	Ala	Glu	Asn	Ile	Lys	Ser	Phe	Leu	
	50					55					60					
Arg	Ser	Phe	Thr	Lys	Leu	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe	
65					70					75					80	
Leu	Leu	Ala	Lys	Lys	Ile	Gln	Thr	Gln	Trp	Lys	Lys	Phe	Gly	Leu	Asp	
				85					90					95		
Ser	Ala	Lys	Leu	Val	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	Asn	Glu	
			100					105						110		
Thr	Asn	Ala	Asn	Tyr	Ile	Ser	Ile	Val	Asp	Glu	His	Glu	Thr	Glu	Ile	
		115					120					125				
Phe	Lys	Thr	Ser	Tyr	Leu	Glu	Pro	Pro	Pro	Asp	Gly	Tyr	Glu	Asn	Val	
	130					135					140					
Thr	Asn	Ile	Val	Pro	Pro	Tyr	Asn	Ala	Phe	Ser	Ala	Gln	Gly	Met	Pro	
145					150					155					160	
Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	Phe	Phe	
			165						170					175		
Lys	Leu	Glu	Arg	Glu	Met	Gly	Ile	Asn	Cys	Thr	Gly	Lys	Ile	Val	Ile	
			180					185					190			
Ala	Arg	Tyr	Gly	Lys	Ile	Phe	Arg	Gly	Asn	Lys	Val	Lys	Asn	Ala	Met	
		195					200						205			
Leu	Ala	Gly	Ala	Ile	Gly	Ile	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	
	210					215					220					
Phe	Ala	Pro	Glu	Val	Gln	Pro	Tyr	Pro	Lys	Gly	Trp	Asn	Leu	Pro	Gly	
225					230					235					240	
Thr	Ala	Ala	Gln	Arg	Gly	Asn	Val	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	
				245				250						255		
Pro	Leu	Thr	Pro	Gly	Tyr	Pro	Ala	Lys	Glu	Tyr	Thr	Phe	Arg	Leu	Asp	
			260					265					270			
Val	Glu	Glu	Gly	Val	Gly	Ile	Pro	Arg	Ile	Pro	Val	His	Pro	Ile	Gly	
		275					280					285				

Tyr	Asn	Asp	Ala	Glu	Ile	Leu	Leu	Arg	Tyr	Leu	Gly	Gly	Ile	Ala	Pro	290	295	300
Pro	Asp	Lys	Ser	Trp	Lys	Gly	Ala	Leu	Asn	Val	Ser	Tyr	Ser	Ile	Gly	305	310	315
Pro	Gly	Phe	Thr	Gly	Ser	Asp	Ser	Phe	Arg	Lys	Val	Arg	Met	His	Val	325	330	335
Tyr	Asn	Ile	Asn	Lys	Ile	Thr	Arg	Ile	Tyr	Asn	Val	Val	Gly	Thr	Ile	340	345	350
Arg	Gly	Ser	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	355	360	365
Asp	Ser	Trp	Val	Phe	Gly	Ala	Ile	Asp	Pro	Thr	Ser	Gly	Val	Ala	Val	370	375	380
Leu	Gln	Glu	Ile	Ala	Arg	Ser	Phe	Gly	Lys	Leu	Met	Ser	Lys	Gly	Trp	385	390	395
Arg	Pro	Arg	Arg	Thr	Ile	Ile	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	405	410	415
Gly	Leu	Leu	Gly	Ser	Thr	Glu	Trp	Ala	Glu	Glu	Asn	Val	Lys	Ile	Leu	420	425	430
Gln	Glu	Arg	Ser	Ile	Ala	Tyr	Ile	Asn	Ser	Asp	Ser	Ser	Ile	Glu	Gly	435	440	445
Asn	Tyr	Thr	Leu	Arg	Val	Asp	Cys	Thr	Pro	Leu	Leu	Tyr	Gln	Leu	Val	450	455	460
Tyr	Lys	Leu	Thr	Lys	Glu	Ile	Pro	Ser	Pro	Asp	Asp	Gly	Phe	Glu	Ser	465	470	475
Lys	Ser	Leu	Tyr	Glu	Ser	Trp	Leu	Glu	Lys	Asp	Pro	Ser	Pro	Glu	Asn	485	490	495
Lys	Asn	Leu	Pro	Arg	Ile	Asn	Lys	Leu	Gly	Ser	Gly	Ser	Asp	Phe	Glu	500	505	510
Ala	Tyr	Phe	Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	515	520	525
Lys	Asn	Lys	Lys	Thr	Asp	Lys	Tyr	Ser	Ser	Tyr	Pro	Val	Tyr	His	Thr	530	535	540
Ile	Tyr	Glu	Thr	Phe	Glu	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Thr	Phe	545	550	555
Lys	Lys	Gln	Leu	Ser	Val	Ala	Gln	Leu	Arg	Gly	Ala	Leu	Val	Tyr	Glu	565	570	575
Leu	Val	Asp	Ser	Lys	Ile	Ile	Pro	Phe	Asn	Ile	Gln	Asp	Tyr	Ala	Glu	580	585	590
Ala	Leu	Lys	Asn	Tyr	Ala	Ala	Ser	Ile	Tyr	Asn	Leu	Ser	Lys	Lys	His			

595		600		605
Asp Gln Gln Leu Thr Asp His Gly Val Ser Phe Asp Ser Leu Phe Ser				
610		615		620
Ala Val Lys Asn Phe Ser Glu Ala Ala Ser Asp Phe His Lys Arg Leu				
625		630		635
Ile Gln Val Asp Leu Asn Asn Pro Ile Ala Val Arg Met Met Asn Asp				
	645		650	655
Gln Leu Met Leu Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro				
	660		665	670
Gly Lys Leu Phe Tyr Arg His Ile Ile Phe Ala Pro Ser Ser His Asn				
	675		680	685
Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Ile Phe Asp				
	690		695	700
Ile Glu Asn Lys Ala Asn Ser Arg Leu Ala Trp Lys Glu Val Lys Lys				
705		710		715
His Ile Ser Ile Ala Ala Phe Thr Ile Gln Ala Ala Ala Gly Thr Leu				
	725		730	735
Lys Glu Val Leu				
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<210> 49

<211> 1860

<212> DNA

<213> Homo sapiens

<400> 49

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aaaaatgaaa ttccttatct tcgcattttt cggtggtggt caccttttat cctgtgctc	180
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ccagaacaga tcctatgagc gattggcact tctggttgat actgttggaac ccagactgag	360
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ccaccacata gaatcaacat atggtaggga ttacagtggg ggcatttctt tatatcacct 1800
cttaaaaaca ttgtttccac tttaaaagta aacacttaat aaatttttgg aagatctctg 1860

<210> 50

<211> 472

<212> PRT

<213> Homo sapiens

<400> 50

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
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Phe	Glu	Glu	Ile	Lys	Glu	Glu	Ile	Ala	Ser	Cys	Gly	Asp	Val	Ala	Lys	35	40	45
Ala	Ile	Ile	Asn	Leu	Ala	Val	Tyr	Gly	Lys	Ala	Gln	Asn	Arg	Ser	Tyr	50	55	60
Glu	Arg	Leu	Ala	Leu	Leu	Val	Asp	Thr	Val	Gly	Pro	Arg	Leu	Ser	Gly	65	70	75
Ser	Lys	Asn	Leu	Glu	Lys	Ala	Ile	Gln	Ile	Met	Tyr	Gln	Asn	Leu	Gln	85	90	95
Gln	Asp	Gly	Leu	Glu	Lys	Val	His	Leu	Glu	Pro	Val	Arg	Ile	Pro	His	100	105	110
Trp	Glu	Arg	Gly	Glu	Glu	Ser	Ala	Val	Met	Leu	Glu	Pro	Arg	Ile	His	115	120	125
Lys	Ile	Ala	Ile	Leu	Gly	Leu	Gly	Ser	Ser	Ile	Gly	Thr	Pro	Pro	Glu	130	135	140
Gly	Ile	Thr	Ala	Glu	Val	Leu	Val	Val	Thr	Ser	Phe	Asp	Glu	Leu	Gln	145	150	155
Arg	Arg	Ala	Ser	Glu	Ala	Arg	Gly	Lys	Ile	Val	Val	Tyr	Asn	Gln	Pro	165	170	175
Tyr	Ile	Asn	Tyr	Ser	Arg	Thr	Val	Gln	Tyr	Arg	Thr	Gln	Gly	Ala	Val	180	185	190
Glu	Ala	Ala	Lys	Val	Gly	Ala	Leu	Ala	Ser	Leu	Ile	Arg	Ser	Val	Ala	195	200	205
Ser	Phe	Ser	Ile	Tyr	Ser	Pro	His	Thr	Gly	Ile	Gln	Glu	Tyr	Gln	Asp	210	215	220
Gly	Val	Pro	Lys	Ile	Pro	Thr	Ala	Cys	Ile	Thr	Val	Glu	Asp	Ala	Glu	225	230	235
Met	Met	Ser	Arg	Met	Ala	Ser	His	Gly	Ile	Lys	Ile	Val	Ile	Gln	Leu	245	250	255
Lys	Met	Gly	Ala	Lys	Thr	Tyr	Pro	Asp	Thr	Asp	Ser	Phe	Asn	Thr	Val	260	265	270
Ala	Glu	Ile	Thr	Gly	Ser	Lys	Tyr	Pro	Glu	Gln	Val	Val	Leu	Val	Ser	275	280	285
Gly	His	Leu	Asp	Ser	Trp	Asp	Val	Gly	Gln	Gly	Ala	Met	Asp	Asp	Gly	290	295	300
Gly	Gly	Ala	Phe	Ile	Ser	Trp	Glu	Ala	Leu	Ser	Leu	Ile	Lys	Asp	Leu	305	310	315
Gly	Leu	Arg	Pro	Lys	Arg	Thr	Leu	Arg	Leu	Val	Leu	Trp	Thr	Ala	Glu	325	330	335

Glu Gln Gly Gly Val Gly Ala Phe Gln Tyr Tyr Gln Leu His Lys Val
340 345 350

Asn Ile Ser Asn Tyr Ser Leu Val Met Glu Ser Asp Ala Gly Thr Phe
355 360 365

Leu Pro Thr Gly Leu Gln Phe Thr Gly Ser Glu Lys Ala Arg Ala Ile
370 375 380

Met Glu Glu Val Met Ser Leu Leu Gln Pro Leu Asn Ile Thr Gln Val
385 390 395 400

Leu Ser His Gly Glu Gly Thr Asp Ile Asn Phe Trp Ile Gln Ala Gly
405 410 415

Val Pro Gly Ala Ser Leu Leu Asp Asp Leu Tyr Lys Tyr Phe Phe Phe
420 425 430

His His Ser His Gly Asp Thr Met Thr Val Met Asp Pro Lys Gln Met
435 440 445

Asn Val Ala Ala Ala Val Trp Ala Val Val Ser Tyr Val Val Ala Asp
450 455 460

Met Glu Glu Met Leu Pro Arg Ser
465 470

<210> 51

<211> 750

<212> PRT

<213> Homo sapiens

<400> 51

Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
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Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
20 25 30

Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
35 40 45

Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
50 55 60

Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His Asn Phe Thr Gln Ile
65 70 75 80

Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
85 90 95

Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His

100					105					110					
Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile
		115					120					125			
Ser	Ile	Ile	Asn	Glu	Asp	Gly	Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe
	130					135					140				
Glu	Pro	Pro	Pro	Pro	Gly	Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro
145					150					155					160
Phe	Ser	Ala	Phe	Ser	Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr
				165					170					175	
Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met
			180					185					190		
Lys	Ile	Asn	Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val
		195					200					205			
Phe	Arg	Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly
	210					215					220				
Val	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys
225					230					235					240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly
				245					250					255	
Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr
			260					265					270		
Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	Ala	Val	Gly
		275					280					285			
Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	Asp	Ala	Gln	Lys
	290					295					300				
Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp	Ser	Ser	Trp	Arg
305					310					315					320
Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Thr	Gly	Asn
				325					330					335	
Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Thr	Asn	Glu	Val
			340					345					350		
Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro
		355					360					365			
Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly
	370					375					380				
Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg
385					390					395					400
Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile
				405					410					415	

Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
420 425 430

Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
435 440 445

Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
450 455 460

Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
465 470 475 480

Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
485 490 495

Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
500 505 510

Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
515 520 525

Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
530 535 540

Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
545 550 555 560

Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
565 570 575

Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
580 585 590

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
595 600 605

Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
610 615 620

Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
625 630 635 640

Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
645 650 655

Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
660 665 670

Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
675 680 685

His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
690 695 700

Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
705 710 715 720

Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
725 730 735

Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
740 745 750

<210> 52

<211> 265

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 52

Thr Lys His Thr Val Ala Thr Val Gly Val Pro Tyr Lys Val Gly Lys
1 5 10 15

Lys Leu Ile Ala Asn Ile Ala Leu Asn Ile Asp Tyr Ser Leu Tyr Phe
20 25 30

Ala Met Asp Ser Tyr Val Glu Phe Ile Lys Thr Gln Asn Ile Ile Ala
35 40 45

Asp Thr Lys His Gly Asp Pro Asp Asn Ile Val Ala Leu Gly Ala His
50 55 60

Ser Asp Ser Val Glu Glu Gly Pro Gly Ile Asn Asp Asp Gly Ser Gly
65 70 75 80

Thr Ile Ser Leu Leu Asn Val Ala Lys Gln Leu Thr His Phe Lys Ile
85 90 95

Asn Asn Lys Val Arg Phe Ala Trp Trp Ala Ala Glu Glu Glu Gly Leu
100 105 110

Leu Gly Ser Asn Phe Tyr Ala Tyr Asn Leu Thr Lys Glu Glu Asn Ser
115 120 125

Lys Ile Arg Val Phe Met Asp Tyr Asp Met Met Ala Ser Pro Asn Tyr
130 135 140

Glu Tyr Glu Ile Tyr Asp Ala Asn Asn Lys Glu Asn Pro Lys Gly Ser
145 150 155 160

Glu Glu Leu Lys Asn Leu Tyr Val Asp Tyr Tyr Lys Ala His His Leu
165 170 175

Asn Tyr Thr Leu Val Pro Phe Asp Gly Arg Ser Asp Tyr Val Gly Phe
180 185 190

Ile Asn Asn Gly Ile Pro Ala Gly Gly Ile Ala Thr Gly Ala Glu Lys
195 200 205

Asn Asn Val Asn Asn Gly Lys Val Leu Asp Arg Cys Tyr His Gln Leu
210 215 220

Cys Asp Asp Val Ser Asn Leu Ser Trp Asp Ala Phe Ile Thr Asn Thr

225		230		235		240									
Lys	Leu	Ile	Ala	His	Ser	Val	Ala	Thr	Tyr	Ala	Asp	Ser	Phe	Glu	Gly
				245					250					255	

Phe	Pro	Lys	Arg	Glu	Thr	Gln	Lys	His
			260					265

<210> 53

<211> 268

<212> PRT

<213> Vibrio cholerae

<400> 53

Gln	Ile	Thr	Asn	Thr	Ile	Arg	Ala	Leu	Ser	Ser	Phe	Asn	Asn	Arg	Phe
1				5					10					15	

Tyr	Thr	Thr	Ala	Ser	Gly	Ala	Gln	Ala	Ser	Asp	Trp	Leu	Ala	Asn	Glu
			20					25					30		

Trp	Arg	Ser	Leu	Ile	Ser	Ser	Leu	Pro	Gly	Ser	Arg	Ile	Glu	Gln	Ile
		35					40					45			

Lys	His	Ser	Gly	Tyr	Asn	Gln	Lys	Ser	Val	Val	Leu	Thr	Ile	Gln	Gly
	50					55					60				

Ser	Glu	Lys	Pro	Asp	Glu	Trp	Val	Ile	Val	Gly	Gly	His	Leu	Asp	Ser
65					70					75					80

Thr	Leu	Gly	Ser	His	Thr	Asn	Glu	Gln	Ser	Ile	Ala	Pro	Gly	Ala	Asp
				85					90					95	

Asp	Asp	Ala	Ser	Gly	Ile	Ala	Ser	Leu	Ser	Glu	Ile	Ile	Arg	Val	Leu
			100					105					110		

Arg	Asp	Asn	Asn	Phe	Arg	Pro	Lys	Arg	Ser	Ala	Ala	Leu	Met	Ala	Tyr
		115					120					125			

Ala	Ala	Glu	Glu	Val	Gly	Leu	Arg	Gly	Ser	Gln	Asp	Pro	Ala	Asn	Gln
		130				135					140				

Tyr	Lys	Ala	Gln	Gly	Lys	Lys	Val	Val	Ser	Val	Leu	Gln	Leu	Asp	Met
145					150					155					160

Thr	Asn	Tyr	Arg	Gly	Ser	Ala	Glu	Asp	Ile	Val	Phe	Ile	Thr	Asp	Tyr
				165					170					175	

Thr	Asp	Ser	Asn	Leu	Thr	Gln	Phe	Leu	Thr	Thr	Leu	Ile	Asp	Glu	Tyr
			180					185					190		

Leu	Pro	Glu	Leu	Thr	Tyr	Gly	Tyr	Asp	Arg	Cys	Gly	Tyr	Ala	Cys	Ser
		195					200					205			

Asp His Ala Ser Trp His Lys Ala Gly Phe Ser Ala Ala Met Pro Phe
210 215 220

Glu Ser Lys Phe Lys Asp Tyr Asn Pro Lys Ile His Thr Ser Gln Asp
225 230 235 240

Thr Leu Ala Asn Ser Asp Pro Thr Gly Asn His Ala Val Thr Phe Thr
245 250 255

Lys Leu Gly Leu Ala Tyr Val Ile Glu Met Ala Asn
260 265

<210> 54

<211> 268

<212> PRT

<213> Aeromonas proteolytica

<400> 54

Gln Ile Thr Gly Thr Ile Ser Ser Leu Glu Ser Phe Thr Asn Arg Phe
1 5 10 15

Tyr Thr Thr Thr Ser Gly Ala Gln Ala Ser Asp Trp Ile Ala Ser Glu
20 25 30

Trp Gln Ala Leu Ser Ala Ser Leu Pro Asn Ala Ser Val Lys Gln Val
35 40 45

Ser His Ser Gly Tyr Asn Gln Lys Ser Val Val Met Thr Ile Thr Gly
50 55 60

Ser Glu Ala Pro Asp Glu Trp Ile Val Ile Gly Gly His Leu Asp Ser
65 70 75 80

Thr Ile Gly Ser His Thr Asn Glu Gln Ser Val Ala Pro Gly Ala Asp
85 90 95

Asp Asp Ala Ser Gly Ile Ala Ala Val Thr Glu Val Ile Arg Val Leu
100 105 110

Ser Glu Asn Asn Phe Gln Pro Lys Arg Ser Ile Ala Phe Met Ala Tyr
115 120 125

Ala Ala Glu Glu Val Gly Leu Arg Gly Ser Gln Asp Leu Ala Asn Gln
130 135 140

Tyr Lys Ser Glu Gly Lys Asn Val Val Ser Ala Leu Gln Leu Asp Met
145 150 155 160

Thr Asn Tyr Lys Gly Ser Ala Gln Asp Val Val Phe Ile Thr Asp Tyr
165 170 175

Thr Asp Ser Asn Phe Thr Gln Tyr Leu Thr Gln Leu Met Asp Glu Tyr
180 185 190

Leu Pro Ser Leu Thr Tyr Gly Phe Asp Thr Cys Gly Tyr Ala Cys Ser
195 200 205

Asp His Ala Ser Trp His Asn Ala Gly Tyr Pro Ala Ala Met Pro Phe
210 215 220

Glu Ser Lys Phe Asn Asp Tyr Asn Pro Arg Ile His Thr Thr Gln Asp
225 230 235 240

Thr Leu Ala Asn Ser Asp Pro Thr Gly Ser His Ala Lys Lys Phe Thr
245 250 255

Gln Leu Gly Leu Ala Tyr Ala Ile Glu Met Gly Ser
260 265

<210> 55

<211> 263

<212> PRT

<213> Streptomyces griseus

<400> 55

Asn Asn Gly Gly Asn Arg Ala His Gly Arg Pro Gly Tyr Lys Ala Ser
1 5 10 15

Val Asp Tyr Val Lys Ala Lys Leu Asp Ala Ala Gly Tyr Thr Thr Thr
20 25 30

Leu Gln Gln Phe Thr Ser Gly Gly Ala Thr Gly Tyr Asn Leu Ile Ala
35 40 45

Asn Trp Pro Gly Gly Asp Pro Asn Lys Val Leu Met Ala Gly Ala His
50 55 60

Leu Asp Ser Val Ser Ser Gly Ala Gly Ile Asn Asp Asn Gly Ser Gly
65 70 75 80

Ser Ala Ala Val Leu Glu Thr Ala Leu Ala Val Ser Arg Ala Gly Tyr
85 90 95

Gln Pro Asp Lys His Leu Arg Phe Ala Trp Trp Gly Ala Glu Glu Leu
100 105 110

Gly Leu Ile Gly Ser Lys Phe Tyr Val Asn Asn Leu Pro Ser Ala Asp
115 120 125

Arg Ser Lys Leu Ala Gly Tyr Leu Asn Phe Asp Met Ile Gly Ser Pro
130 135 140

Asn Pro Gly Tyr Phe Val Tyr Asp Asp Asp Pro Val Ile Glu Lys Thr
145 150 155 160

Phe Lys Asn Tyr Phe Ala Gly Leu Asn Val Pro Thr Glu Ile Glu Thr

				165						170						175
Glu	Gly	Asp	Gly	Arg	Ser	Asp	His	Ala	Pro	Phe	Lys	Asn	Val	Gly	Val	
			180					185					190			
Pro	Val	Gly	Gly	Leu	Phe	Thr	Gly	Ala	Gly	Tyr	Thr	Lys	Ser	Ala	Ala	
		195					200					205				
Gln	Ala	Gln	Lys	Trp	Gly	Gly	Thr	Ala	Gly	Gln	Ala	Phe	Asp	Arg	Cys	
	210					215					220					
Tyr	His	Ser	Ser	Cys	Asp	Ser	Leu	Ser	Asn	Ile	Asn	Asp	Thr	Ala	Leu	
225					230					235					240	
Asp	Arg	Asn	Ser	Asp	Ala	Ala	Ala	His	Ala	Ile	Trp	Thr	Leu	Ser	Ser	
				245					250						255	
Gly	Thr	Gly	Glu	Pro	Pro	Thr										
			260													

<210> 56

<211> 282

<212> PRT

<213> Homo sapiens

<400> 56

Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp
1				5					10					15	
Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly
			20					25					30		
Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser
		35					40					45			
Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly
	50					55					60				
Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser
65					70					75				80	
Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His
				85					90					95	
Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro
			100					105					110		
Arg	Arg	Thr	Ile	Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu
		115					120						125		
Leu	Gly	Ser	Thr	Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu
	130					135					140				

Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr
145 150 155 160
Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn
165 170 175
Leu Thr Lys Glu Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser
180 185 190
Leu Tyr Glu Ser Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly
195 200 205
Met Pro Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe
210 215 220
Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn
225 230 235 240
Trp Glu Thr Asn Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr
245 250 255
Glu Thr Tyr Glu Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr
260 265 270
His Leu Thr Val Ala Gln Val Arg Gly Gly
275 280

<210> 57

<211> 282

<212> PRT

<213> Homo sapiens

<400> 57

Asp Ala Glu Ile Leu Leu Arg Tyr Leu Gly Gly Ile Ala Pro Pro Asp
1 5 10 15
Lys Ser Trp Lys Gly Ala Leu Asn Val Ser Tyr Ser Ile Gly Pro Gly
20 25 30
Phe Thr Gly Ser Asp Ser Phe Arg Lys Val Arg Met His Val Tyr Asn
35 40 45
Ile Asn Lys Ile Thr Arg Ile Tyr Asn Val Val Gly Thr Ile Arg Gly
50 55 60
Ser Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser
65 70 75 80
Trp Val Phe Gly Ala Ile Asp Pro Thr Ser Gly Val Ala Val Leu Gln
85 90 95
Glu Ile Ala Arg Ser Phe Gly Lys Leu Met Ser Lys Gly Trp Arg Pro
100 105 110

Arg Arg Thr Ile Ile Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu
115 120 125

Leu Gly Ser Thr Glu Trp Ala Glu Glu Asn Val Lys Ile Leu Gln Glu
130 135 140

Arg Ser Ile Ala Tyr Ile Asn Ser Asp Ser Ser Ile Glu Gly Asn Tyr
145 150 155 160

Thr Leu Arg Val Asp Cys Thr Pro Leu Leu Tyr Gln Leu Val Tyr Lys
165 170 175

Leu Thr Lys Glu Ile Pro Ser Pro Asp Asp Gly Phe Glu Ser Lys Ser
180 185 190

Leu Tyr Glu Ser Trp Leu Glu Lys Asp Pro Ser Pro Glu Asn Lys Asn
195 200 205

Leu Pro Arg Ile Asn Lys Leu Gly Ser Gly Ser Asp Phe Glu Ala Tyr
210 215 220

Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn
225 230 235 240

Lys Lys Thr Asp Lys Tyr Ser Ser Tyr Pro Val Tyr His Thr Ile Tyr
245 250 255

Glu Thr Phe Glu Leu Val Glu Lys Phe Tyr Asp Pro Thr Phe Lys Lys
260 265 270

Gln Leu Ser Val Ala Gln Leu Arg Gly Ala
275 280

<210> 58

<211> 283

<212> PRT

<213> Homo sapiens

<400> 58

Arg Asp Leu Leu Cys Asn Leu Asn Gly Thr Leu Ala Pro Ala Thr Trp
1 5 10 15

Gln Gly Ala Leu Gly Cys His Tyr Arg Leu Gly Pro Gly Phe Arg Pro
20 25 30

Asp Gly Asp Phe Pro Ala Asp Ser Gln Val Asn Val Ser Val Tyr Asn
35 40 45

Arg Leu Glu Leu Arg Asn Ser Ser Asn Val Leu Gly Ile Ile Arg Gly
50 55 60

Ala Val Glu Pro Asp Arg Tyr Val Leu Tyr Gly Asn His Arg Asp Ser

65		70		75		80
Trp Val His Gly	Ala Val Asp Pro Ser Ser Gly Thr Ala Val Leu Leu	85	90	95		
Glu Leu Ser Arg	Val Leu Gly Thr Leu Leu Lys Lys Gly Thr Trp Arg	100	105	110		
Pro Arg Arg Ser	Ile Val Phe Ala Ser Trp Gly Ala Glu Glu Phe Gly	115	120	125		
Leu Ile Gly Ser	Thr Glu Phe Thr Glu Glu Phe Phe Asn Lys Leu Gln	130	135	140		
Glu Arg Thr Val	Ala Tyr Ile Asn Val Asp Ile Ser Val Phe Ala Asn	145	150	155	160	
Ala Thr Leu Arg	Val Gln Gly Thr Pro Pro Val Gln Ser Val Val Phe	165	170	175		
Ser Ala Thr Lys	Glu Ile Arg Ser Pro Gly Pro Gly Asp Leu Ser Ile	180	185	190		
Tyr Asp Asn Trp	Ile Arg Tyr Phe Asn Arg Ser Ser Pro Val Tyr Gly	195	200	205		
Leu Val Pro Ser	Leu Gly Ser Leu Gly Ala Gly Ser Asp Tyr Ala Pro	210	215	220		
Phe Val His Phe	Leu Gly Ile Ser Ser Met Asp Ile Ala Tyr Thr Tyr	225	230	235	240	
Asp Arg Ser Lys	Thr Ser Ala Arg Ile Tyr Pro Thr Tyr His Thr Ala	245	250	255		
Phe Asp Thr Phe	Asp Tyr Val Asp Lys Phe Leu Asp Pro Gly Phe Ser	260	265	270		
Ser His Gln Ala	Val Ala Arg Thr Ala Gly Ser	275	280			

<210> 59

<211> 259

<212> PRT

<213> Homo sapiens

<400> 59

Ser Pro His Thr	Gly Ile Gln Glu Tyr Gln Asp Gly Val Pro Lys Ile	1	5	10	15
Pro Thr Ala Cys	Ile Thr Val Glu Asp Ala Glu Met Met Ser Arg Met	20	25	30	

Ala	Ser	His	Gly	Ile	Lys	Ile	Val	Ile	Gln	Leu	Lys	Met	Gly	Ala	Lys
		35					40					45			
Thr	Tyr	Pro	Asp	Thr	Asp	Ser	Phe	Asn	Thr	Val	Ala	Glu	Ile	Thr	Gly
		50				55					60				
Ser	Lys	Tyr	Pro	Glu	Gln	Val	Val	Leu	Val	Ser	Gly	His	Leu	Asp	Ser
65					70					75					80
Trp	Asp	Val	Gly	Gln	Gly	Ala	Met	Asp	Asp	Gly	Gly	Gly	Ala	Phe	Ile
				85					90					95	
Ser	Trp	Glu	Ala	Leu	Ser	Leu	Ile	Lys	Asp	Leu	Gly	Leu	Arg	Pro	Lys
			100					105					110		
Arg	Thr	Leu	Arg	Leu	Val	Leu	Trp	Thr	Ala	Glu	Glu	Gln	Gly	Gly	Val
		115					120					125			
Gly	Ala	Phe	Gln	Tyr	Tyr	Gln	Leu	His	Lys	Val	Asn	Ile	Ser	Asn	Tyr
		130				135					140				
Ser	Leu	Val	Met	Glu	Ser	Asp	Ala	Gly	Thr	Phe	Leu	Pro	Thr	Gly	Leu
145					150					155					160
Gln	Phe	Thr	Gly	Ser	Glu	Lys	Ala	Arg	Ala	Ile	Met	Glu	Glu	Val	Met
				165					170					175	
Ser	Leu	Leu	Gln	Pro	Leu	Asn	Ile	Thr	Gln	Val	Leu	Ser	His	Gly	Glu
			180					185					190		
Gly	Thr	Asp	Ile	Asn	Phe	Trp	Ile	Gln	Ala	Gly	Val	Pro	Gly	Ala	Ser
		195					200					205			
Leu	Leu	Asp	Asp	Leu	Tyr	Lys	Tyr	Phe	Phe	Phe	His	His	Ser	His	Gly
		210				215					220				
Asp	Thr	Met	Thr	Val	Met	Asp	Pro	Lys	Gln	Met	Asn	Val	Ala	Ala	Ala
225					230					235					240
Val	Trp	Ala	Val	Val	Ser	Tyr	Val	Val	Ala	Asp	Met	Glu	Glu	Met	Leu
				245					250					255	
Pro	Arg	Ser													

FIG. 8

NAALAD I DAQKLEKNGGSAPPD--SSURGSLKVPINVGPGFTGNF---STQKVKEHIHSTNEVTRIYVIGTUTRGAVEPDRYVILGG 375
 NAALAD II DAEILLRYLGGIAPPD--KSUKGALNVSISIGPGFTGSD---SFRKVRCHVYNINKITRIYVVGITRGSVEDPDRYVILGG 366
 NAALAD L --RDLLCNLNGTLAP--ATUQGALGCHYRLGPGFRPDGFPADSQVNVSVYNRLELRNSSLVULGIIRGAVEPDRYVILYEN 367
 NAALAD IV SPHTGQOEYQDGVKPIKTACITVEDAEHNSRHASHGIK---IVIQLKCAKTYPDIDS-FVIVAEITGSKYPEQVWLVS 289
 APE 3 yeast -----TKHTVATVGVPYKVGKKLIANIALNIDYSLYFANDSYVEFIKTQLIADTKHG-DPILNIVLALGA 313
 P96152 QITNTIRALSSFNRFYTTASGAQASDMLANEURSLIS---SLPGSRHEQIKHSGVNO-KSVNLTIQSEKPDENVIVGG 199
 AMPX vibpr QITGTSSLESFTNRFYTTTSGAQASDMLIASEUQALSA---SLPNASVKQVSHSGVNO-KSVNHTITGSEAPDEVIVIVGG 202
 APX Strgr -----NNGGNR--AHGRPGYKASVDYVKAKLDA--GYTTTQQFTSGGATG-YULIANUPCG-DPNKVLHAGA 84

NAALAD I HRDSU-VF-----G-TI-DPQSG-EAV-VHEVMSFGTL-KKEG-RRPRRTILFASMDNEEFGLLGSTETA-EE-NS 439
 NAALAD II HRDSU-VF-----G-AI-DPTSG-VAV-LOEHLNDSFCKL-HSKG-RRPRRTILFASMDNEEFGLLGSTETA-EE-NV 429
 NAALAD L HRDSU-VH-----GAV--DPSGTVL-L-ELSEVLTLLK-KGTWPPRSIVFASMGREEFGLIGSTEFT-EEFFN 432
 NAALAD IV HLDSNDV-----CGAMDGCG-DFISU-EALSLL-----KDLG-LRPHRTLRVLMTREECGGVCFAQYI-QLHKV 352
 APE 3 yeast HSDS--VEE-----EPGINDDCGCTISL-L-NVLRQLTH-----FKNNKVRFAUWMAHEEGLIGSNFAYNLTKE 375
 P96152 HLDSST-LGSHTNEQSIAPGADDDASGIESL-S-EIIRVL-----RDNN-FRPRRSIALHAYANEEVGLRGSDPA-NQYKA 270
 AMPX vibpr HLDSST-IGSHTNEQSVAPGADDDASGIRAV-T-EVIEVL-----SENN-FQPKRSIAFMAYANEEVGLRGSDLA-NQYKS 273
 APX Strgr HLDS--VSS-----GAGINDNGSGSAAV-L-ETALLV-----SRAG-YQPDHMLRFAUWMAHEEGLIGSKFIV-NNLPS 147

NAALAD I RLLQERGVAYINADSSI-EGNYTLRQDCDPLHYSLVHNLKELKSPDECFEGKSLYESUTKKS--PSPEFSGHPRISKLG 516
 NAALAD II KILQERSIAYINADSSI-EGNYTLRQDCDPLLYQLVYKLVKEIPSPDDGFEKSLYESULEKD--PSPENKNLPRINKLG 506
 NAALAD L KL-QEPTVAYINADISV-FANATLRQCPPPVQSVVFSAMKEIRSPGPGD--LSIYDNTIRYFNRRSSPVYGLVPSLGSLS 508
 NAALAD IV NIS--NYSLVNESQAGT-FLPTGLOFTCEKARA---INEEVM-----SLQPLNITQ-----VLSHG 404
 APE 3 yeast ENSKIR--VFDDYDHMA-SPNYEVEHYDANKENP--KGEELK-----NLVVDVYKAH-----HLNYTLVPFDG 435
 P96152 QGK--KQVSVLQLOMTNYRGSIEDIFIDYDTS---NLIQFLT-----TLIDEVLPEL-----TYG-----YDRCG 327
 AMPX vibpr EGK--NVVSALQLOMTNYKGSAQDVVFIIDYDTS---NFIQYLT-----QLHDEFLPSL-----TYG-----FDTGG 330
 APX Strgr AD-RSELAGYLNFM-IGSPNPGYFYDDDPVIEK--TFKNYFAG-----LNVPTETETE-----GDGRSDHAPFKN 210

FIG. 8. (CONTINUED)

NAALAD I	★	SGNDFEVF	QRL	IASGRARYT	NUETNKF	SGYPLYH	SVYEL	VEK	---	FYDPH	KYH	---	LTV	QVRGG	---	582				
NAALAD II		SGSDFEAY	QRL	IASGRARYT	NKKTKYSS	YPVYH	YIYEF	FEL	VEK	---	FYDPT	KKQ	---	LSV	QLRGA	---	572			
NAALAD L		AGSDYAPF	VHFL	ISSHDIA	YTYDRSKT	SARIYPT	YHJAF	DFDY	VDK	---	FLDPG	SSH	---	QAV	RTAGS	---	574			
NAALAD IV		EGTDIN	---	FQ	IQACVPGAS	LLDDL	YKYFF	---	---	---	FHS	HGD	---	MTV	DPKQMN	VAAV	---	472		
APX 3 yeast		RSDYVGF	INNGIP	AGGIATGA	EKNVNN	NGKVL	DRCYH	QLC	DVSN	---	SUDAF	ITNTK	---	LIAH	SVATV	DSFEG	PKRETQKH	---	515	
P96152		YACSDHAS	---	HKAC	FSA	AHPFES	---	---	---	---	PKI	---	---	---	---	---	---	---	391	
AMPX vibpr		YACSDHAS	---	CHNAC	GYP	AHPFES	---	---	---	---	PRH	---	---	---	---	---	---	---	394	
APX strgr		VGVPVGG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	284